

## RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 09/804,625A  
Source: TFW16  
Date Processed by STIC: 3-1-05

# ***ENTERED***



RAW SEQUENCE LISTING DATE: 03/01/2005  
 PATENT APPLICATION: US/09/804,625A TIME: 07:59:37

Input Set : A:\87023902.app  
 Output Set: N:\CRF4\03012005\I804625A.raw

```

66 cct tta tat gtg gac ttc agt gat gtg ggg tgg aat gac tgg atc gtt 144
67 Pro Leu Tyr Val Asp Phe Ser Asp Val Gly Trp Asn Asp Trp Ile Val
68      35      40      45
70 gca ccg ccg ggg tat cat gcc ttt tac tgc cat ggg gag tgc cct ttt 192
71 Ala Pro Pro Gly Tyr His Ala Phe Tyr Cys His Gly Glu Cys Pro Phe
72      50      55      60
74 ccc ctg gcc gat cac ctt aac tcc acg aat cat gcc att ctc caa act 240
75 Pro Leu Ala Asp His Leu Asn Ser Thr Asn His Ala Ile Leu Gln Thr
76 65      70      75      80
78 ctg gtc aac tca gtt aac tct aag att ccc aag gca tgc tgt gtc cca 288
79 Leu Val Asn Ser Val Asn Ser Lys Ile Pro Lys Ala Cys Cys Val Pro
80      85      90      95
82 aca gag ctc agc gcc atc tcc atg ctg tac ctt gat gag aat gag aag 336
83 Thr Glu Leu Ser Ala Ile Ser Met Leu Tyr Leu Asp Glu Asn Glu Lys
84      100      105      110
86 gtg gta tta aag aac tat cag gac atg ggt gtc gag ggt tgt ggg tgt 384
87 Val Val Leu Lys Asn Tyr Gln Asp Met Gly Val Glu Gly Cys Gly Cys
88      115      120      125
90 cgt tagcacagca aaataaaata taaatatata tatatatata ttagaaaaaac 437
91 Arg
93 agcaaaaaaaaa tcaagttgac actttaatat ttcccaatga agactttatt tatggaatgg 497
95 aatggagaaaa aagaaaaaca cagctatattt gaaaactata tttatatcta ccgaaaagaa 557
97 gttgggaaaaa caaatatattt aatcagagaa ttatt 592
100 <210> SEQ ID NO: 2
101 <211> LENGTH: 129
102 <212> TYPE: PRT
103 <213> ORGANISM: Bos taurus
105 <400> SEQUENCE: 2
106 Gly His Asp Gly Lys Gly His Pro Leu His Arg Arg Glu Lys Arg Gln
107 1      5      10      15
109 Ala Lys His Lys Gln Arg Lys Arg Leu Lys Ser Ser Cys Lys Arg His
110      20      25      30
112 Pro Leu Tyr Val Asp Phe Ser Asp Val Gly Trp Asn Asp Trp Ile Val
113      35      40      45
115 Ala Pro Pro Gly Tyr His Ala Phe Tyr Cys His Gly Glu Cys Pro Phe
116      50      55      60
118 Pro Leu Ala Asp His Leu Asn Ser Thr Asn His Ala Ile Leu Gln Thr
119 65      70      75      80
121 Leu Val Asn Ser Val Asn Ser Lys Ile Pro Lys Ala Cys Cys Val Pro
122      85      90      95
124 Thr Glu Leu Ser Ala Ile Ser Met Leu Tyr Leu Asp Glu Asn Glu Lys
125      100      105      110
127 Val Val Leu Lys Asn Tyr Gln Asp Met Gly Val Glu Gly Cys Gly Cys
128      115      120      125
130 Arg
135 <210> SEQ ID NO: 3
136 <211> LENGTH: 1607
137 <212> TYPE: DNA
138 <213> ORGANISM: Homo sapiens

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140 <220> FEATURE:
141 <221> NAME/KEY: CDS
142 <222> LOCATION: (356)..(1543)
144 <400> SEQUENCE: 3
145 gtcgactcta gagtgtgtgt cagcacttgg ctggggactt cttgaacttg cagggagaat 60
147 aacttgcgca cccacttttg cgccggtgcc ttggccccag cggagcctgc ttcgccatct 120
149 ccgagcccca ccgcccctcc actcctcggc cttgcccgcac actgagacgc tgttcccagc 180
151 gtgaaaagag agactgcgcg gccggcaccg gggagaagga ggaggcaaag aaaaggaacg 240
153 gacattcggt ccttgcgcca ggtcctttga ccagagtttt tccatgtgga cgctctttca 300
155 atggacgtgt ccccgcgctgc ttcttagacg gactgcggtc tcctaaaggt cgacc atg 358
156 Met
157 1
159 gtg gcc ggg acc cgc tgt ctt cta gcg ttg ctg ctt ccc cag gtc ctc 406
160 Val Ala Gly Thr Arg Cys Leu Leu Ala Leu Leu Leu Pro Gln Val Leu
161 5 10 15
163 ctg ggc ggc gcg gct ggc ctc gtt ccg gag ctg ggc cgc agg aag ttc 454
164 Leu Gly Gly Ala Ala Gly Leu Val Pro Glu Leu Gly Arg Arg Lys Phe
165 20 25 30
167 gcg gcg gcg tcg tcg ggc cgc ccc tca tcc cag ccc tct gac gag gtc 502
168 Ala Ala Ala Ser Ser Gly Arg Pro Ser Ser Gln Pro Ser Asp Glu Val
169 35 40 45
171 ctg agc gag ttc gag ttg cgg ctg ctc agc atg ttc ggc ctg aaa cag 550
172 Leu Ser Glu Phe Glu Leu Arg Leu Leu Ser Met Phe Gly Leu Lys Gln
173 50 55 60 65
175 aga ccc acc ccc agc agg gac gcc gtg gtg ccc ccc tac atg cta gac 598
176 Arg Pro Thr Pro Ser Arg Asp Ala Val Val Pro Pro Tyr Met Leu Asp
177 70 75 80
179 ctg tat cgc agg cac tca ggt cag ccg ggc tca ccc gcc cca gac cac 646
180 Leu Tyr Arg Arg His Ser Gly Gln Pro Gly Ser Pro Ala Pro Asp His
181 85 90 95
183 cgg ttg gag agg gca gcc agc cga gcc aac act gtg cgc agc ttc cac 694
184 Arg Leu Glu Arg Ala Ala Ser Arg Ala Asn Thr Val Arg Ser Phe His
185 100 105 110
187 cat gaa gaa tct ttg gaa gaa cta cca gaa acg agt ggg aaa aca acc 742
188 His Glu Glu Ser Leu Glu Glu Leu Pro Glu Thr Ser Gly Lys Thr Thr
189 115 120 125
191 cgg aga ttc ttc ttt aat tta agt tct atc ccc acg gag gag ttt atc 790
192 Arg Arg Phe Phe Phe Asn Leu Ser Ser Ile Pro Thr Glu Glu Phe Ile
193 130 135 140 145
195 acc tca gca gag ctt cag gtt ttc cga gaa cag atg caa gat gct tta 838
196 Thr Ser Ala Glu Leu Gln Val Phe Arg Glu Gln Met Gln Asp Ala Leu
197 150 155 160
199 gga aac aat agc agt ttc cat cac cga att aat att tat gaa atc ata 886
200 Gly Asn Asn Ser Ser Phe His His Arg Ile Asn Ile Tyr Glu Ile Ile
201 165 170 175
203 aaa cct gca aca gcc aac tcg aaa ttc ccc gtg acc aga ctt ttg gac 934
204 Lys Pro Ala Thr Ala Asn Ser Lys Phe Pro Val Thr Arg Leu Leu Asp
205 180 185 190
207 acc agg ttg gtg aat cag aat gca agc agg tgg gaa agt ttt gat gtc 982

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208 Thr Arg Leu Val Asn Gln Asn Ala Ser Arg Trp Glu Ser Phe Asp Val
209      195                200                205
211 acc ccc gct gtg atg cgg tgg act gca cag gga cac gcc aac cat gga 1030
212 Thr Pro Ala Val Met Arg Trp Thr Ala Gln Gly His Ala Asn His Gly
213 210                215                220                225
215 ttc gtg gtg gaa gtg gcc cac ttg gag gag aaa caa ggt gtc tcc aag 1078
216 Phe Val Val Glu Val Ala His Leu Glu Glu Lys Gln Gly Val Ser Lys
217                230                235                240
219 aga cat gtt agg ata agc agg tct ttg cac caa gat gaa cac agc tgg 1126
220 Arg His Val Arg Ile Ser Arg Ser Leu His Gln Asp Glu His Ser Trp
221                245                250                255
223 tca cag ata agg cca ttg cta gta act ttt ggc cat gat gga aaa ggg 1174
224 Ser Gln Ile Arg Pro Leu Leu Val Thr Phe Gly His Asp Gly Lys Gly
225                260                265                270
227 cat cct ctc cac aaa aga gaa aaa cgt caa gcc aaa cac aaa cag cgg 1222
228 His Pro Leu His Lys Arg Glu Lys Arg Gln Ala Lys His Lys Gln Arg
229      275                280                285
231 aaa cgc ctt aag tcc agc tgt aag aga cac cct ttg tac gtg gac ttc 1270
232 Lys Arg Leu Lys Ser Ser Cys Lys Arg His Pro Leu Tyr Val Asp Phe
233 290                295                300                305
235 agt gac gtg ggg tgg aat gac tgg att gtg gct ccc ccg ggg tat cac 1318
236 Ser Asp Val Gly Trp Asn Asp Trp Ile Val Ala Pro Pro Gly Tyr His
237                310                315                320
239 gcc ttt tac tgc cac gga gaa tgc cct ttt cct ctg gct gat cat ctg 1366
240 Ala Phe Tyr Cys His Gly Glu Cys Pro Phe Pro Leu Ala Asp His Leu
241                325                330                335
243 aac tcc act aat cat gcc att gtt cag acg ttg gtc aac tct gtt aac 1414
244 Asn Ser Thr Asn His Ala Ile Val Gln Thr Leu Val Asn Ser Val Asn
245      340                345                350
247 tct aag att cct aag gca tgc tgt gtc ccg aca gaa ctc agt gct atc 1462
248 Ser Lys Ile Pro Lys Ala Cys Cys Val Pro Thr Glu Leu Ser Ala Ile
249      355                360                365
251 tcg atg ctg tac ctt gac gag aat gaa aag gtt gta tta aag aac tat 1510
252 Ser Met Leu Tyr Leu Asp Glu Asn Glu Lys Val Val Leu Lys Asn Tyr
253 370                375                380                385
255 cag gac atg gtt gtg gag ggt tgt ggg tgt cgc tagtacagca aaattaaata 1563
256 Gln Asp Met Val Val Glu Gly Cys Gly Cys Arg
257                390                395
259 cataaatata tatatatata tatatttttag aaaaaagaaa aaaa 1607
262 <210> SEQ ID NO: 4
263 <211> LENGTH: 396
264 <212> TYPE: PRT
265 <213> ORGANISM: Homo sapiens
267 <400> SEQUENCE: 4
268 Met Val Ala Gly Thr Arg Cys Leu Leu Ala Leu Leu Leu Pro Gln Val
269 1 5 10 15
271 Leu Leu Gly Gly Ala Ala Gly Leu Val Pro Glu Leu Gly Arg Arg Lys
272 20 25 30
274 Phe Ala Ala Ala Ser Ser Gly Arg Pro Ser Ser Gln Pro Ser Asp Glu

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```

275          35          40          45
277 Val Leu Ser Glu Phe Glu Leu Arg Leu Leu Ser Met Phe Gly Leu Lys
278          50          55          60
280 Gln Arg Pro Thr Pro Ser Arg Asp Ala Val Val Pro Pro Tyr Met Leu
281 65          70          75          80
283 Asp Leu Tyr Arg Arg His Ser Gly Gln Pro Gly Ser Pro Ala Pro Asp
284          85          90          95
286 His Arg Leu Glu Arg Ala Ala Ser Arg Ala Asn Thr Val Arg Ser Phe
287          100          105          110
289 His His Glu Ser Leu Glu Glu Leu Pro Glu Thr Ser Gly Lys Thr
290          115          120          125
292 Thr Arg Arg Phe Phe Phe Asn Leu Ser Ser Ile Pro Thr Glu Glu Phe
293 130          135          140
295 Ile Thr Ser Ala Glu Leu Gln Val Phe Arg Glu Gln Met Gln Asp Ala
296 145          150          155          160
298 Leu Gly Asn Asn Ser Ser Phe His His Arg Ile Asn Ile Tyr Glu Ile
299          165          170          175
301 Ile Lys Pro Ala Thr Ala Asn Ser Lys Phe Pro Val Thr Arg Leu Leu
302          180          185          190
304 Asp Thr Arg Leu Val Asn Gln Asn Ala Ser Arg Trp Glu Ser Phe Asp
305          195          200          205
307 Val Thr Pro Ala Val Met Arg Trp Thr Ala Gln Gly His Ala Asn His
308 210          215          220
310 Gly Phe Val Val Glu Val Ala His Leu Glu Glu Lys Gln Gly Val Ser
311 225          230          235          240
313 Lys Arg His Val Arg Ile Ser Arg Ser Leu His Gln Asp Glu His Ser
314          245          250          255
316 Trp Ser Gln Ile Arg Pro Leu Leu Val Thr Phe Gly His Asp Gly Lys
317          260          265          270
319 Gly His Pro Leu His Lys Arg Glu Lys Arg Gln Ala Lys His Lys Gln
320          275          280          285
322 Arg Lys Arg Leu Lys Ser Ser Cys Lys Arg His Pro Leu Tyr Val Asp
323          290          295          300
325 Phe Ser Asp Val Gly Trp Asn Asp Trp Ile Val Ala Pro Pro Gly Tyr
326 305          310          315          320
328 His Ala Phe Tyr Cys His Gly Glu Cys Pro Phe Pro Leu Ala Asp His
329          325          330          335
331 Leu Asn Ser Thr Asn His Ala Ile Val Gln Thr Leu Val Asn Ser Val
332          340          345          350
334 Asn Ser Lys Ile Pro Lys Ala Cys Cys Val Pro Thr Glu Leu Ser Ala
335          355          360          365
337 Ile Ser Met Leu Tyr Leu Asp Glu Asn Glu Lys Val Val Leu Lys Asn
338          370          375          380
340 Tyr Gln Asp Met Val Val Glu Gly Cys Gly Cys Arg
341 385          390          395
345 <210> SEQ ID NO: 5
346 <211> LENGTH: 1954
347 <212> TYPE: DNA
348 <213> ORGANISM: Homo sapiens

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RAW SEQUENCE LISTING ERROR SUMMARY      DATE: 03/01/2005  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:14; Xaa Pos. 6  
Seq#:15; N Pos. 3  
Seq#:16; N Pos. 12,15

VERIFICATION SUMMARY

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L:653 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:0

L:671 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:0

L:693 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:0